



1

# SEQUENCE LISTING

<110> ROUX, SYLVIE  
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<120> IN VIVO MODULATION OF NEURONAL TRANSPORT

<130> 03495.0174-02000

<140> 10/662,808

<141> 2003-09-16

<150> 09/816,467

<151> 2001-03-26

<150> 09/129,368

<151> 1998-08-05

<150> 60/055,615

<151> 1997-08-14

<150> 60/065,236

<151> 1997-11-13

<160> 18

<170> PatentIn Ver. 3.2

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<212> DNA

<213> Clostridium tetani

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<222> (88)..(1476)

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Met Val Phe Ser Thr Pro Ile Pro Phe

1

5

tct tat tct aaa aat ctg gat tgt tgg gtt gat aat gaa gaa gat ata 162

Ser Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile

10

15

20

25

gat gtt ata tta aaa aag agt aca att tta aat tta gat att aat aat 210

Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn

30

35

40

gat att ata tca gat ata tct ggg ttt aat tca tct gta ata aca tat 258

Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr

45

50

55

cca gat gct caa ttg gtg ccc gga ata aat ggc aaa gca ata cat tta	306
Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu	
60 65 70	
gta aac aat gaa tct tct gaa gtt ata gtg cat aaa gct atg gat att	354
Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile	
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gaa tat aat gat atg ttt aat aat ttt acc gtt agc ttt tgg ttg agg	402
Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg	
90 95 100 105	
gtt cct aaa gta tct gct agt cat tta gaa caa tat ggc aca aat gag	450
Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu	
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tat tca ata att agc tct atg aaa aaa cat agt cta tca ata gga tct	498
Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser	
125 130 135	
ggg tgg agt gta tca ctt aaa ggt aat aac tta ata tgg act tta aaa	546
Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys	
140 145 150	
gat tcc gcg gga gaa gtt aga caa ata act ttt agg gat tta cct gat	594
Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp	
155 160 165	
aaa ttt aat gct tat tta gca aat aaa tgg gtt ttt ata act att act	642
Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr	
170 175 180 185	
aat gat aga tta tct tct gct aat ttg tat ata aat gga gta ctt atg	690
Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met	
190 195 200	
gga agt gca gaa att act ggt tta gga gct att aga gag gat aat aat	738
Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn	
205 210 215	
ata aca tta aaa cta gat aga tgt aat aat aat aat caa tac gtt tct	786
Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser	
220 225 230	
att gat aaa ttt agg ata ttt tgc aaa gca tta aat cca aaa gag att	834
Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile	
235 240 245	
gaa aaa tta tac aca agt tat tta tct ata acc ttt tta aga gac ttc	882
Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe	
250 255 260 265	
tgg gga aac cct tta cga tat gat aca gaa tat tat tta ata cca gta	930
Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val	
270 275 280	

gct tct agt tct aaa gat gtt caa ttg aaa aat ata aca gat tat atg 978  
 Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met  
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tat ttg aca aat gcg cca tcg tat act aac gga aaa ttg aat ata tat 1026  
 Tyr Leu Thr Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile Tyr  
 300 305 310

tat aga agg tta tat aat gga cta aaa ttt att ata aaa aga tat aca 1074  
 Tyr Arg Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr  
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 Pro Asn Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys  
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 Asn Ala Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu  
 380 385 390

cgt gat tta aaa acc tat tct gta caa ctt aaa tta tat gat gat aaa 1314  
 Arg Asp Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys  
 395 400 405

aat gca tct tta gga cta gta ggt acc cat aat ggt caa ata ggc aac 1362  
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gat cca aat agg gat ata tta att gca agc aac tgg tac ttt aat cat 1410  
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 430 435 440

tta aaa gat aaa att tta gga tgt gat tgg tac ttt gta cct aca gat 1458  
 Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp  
 445 450 455

gag gga tgg aca aat gat taaacagatt gatattgttca tgacatatgc 1506  
 Glu Gly Trp Thr Asn Asp  
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&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Clostridium tetani

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Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser  
 35 40 45

Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro  
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Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu  
 65 70 75 80

Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn  
 85 90 95

Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser  
 100 105 110

His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met  
 115 120 125

Lys Lys His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys  
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Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg  
 145 150 155 160

Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala  
 165 170 175

Asn Lys Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala  
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Asn Leu Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly  
 195 200 205

Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg  
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Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe  
 225 230 235 240

Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr  
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Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr  
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Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val  
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Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser  
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Tyr Thr Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly  
 305 310 315 320  
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 340 345 350  
 Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe Asn Asn  
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 Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu Lys Thr Tyr Ser  
 385 390 395 400  
 Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser Leu Gly Leu Val  
 405 410 415  
 Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro Asn Arg Asp Ile Leu  
 420 425 430  
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 caattgggtgc ccggaataaa tggcaaagca atacatttag taaacaatga atcttctgaa 240  
 gttatagtgc ataaagctat ggatattgaa tataatgata tgtttaataa ttttaccgtt 300  
 agcttttggg tgagggttcc taaagtatct gctagtcatt tagaacaata tggcacaaat 360  
 gagtattcaa taattagctc tatgaaaaaa catagtctat caataggatc tggttggagt 420  
 gtatcactta aaggaataaa cttaatatgg actttaaaag attccgcggg agaagttaga 480  
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 aatgcgccat cgtatactaa cggaaaattg aatatatatt atagaagggt atataatgga 960  
 ctaaaattta ttataaaaag atatacacct aataatgaaa tagattcttt tgttaaata 1020  
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 aaagatggaa atgcctttaa taatcttgat agaattctaa gagtaggtta taatgcccc 1140  
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gtacaactta aattatatga tgataaaaaat gcatctttag gactagtagg tacccataat 1260  
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<210> 18  
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